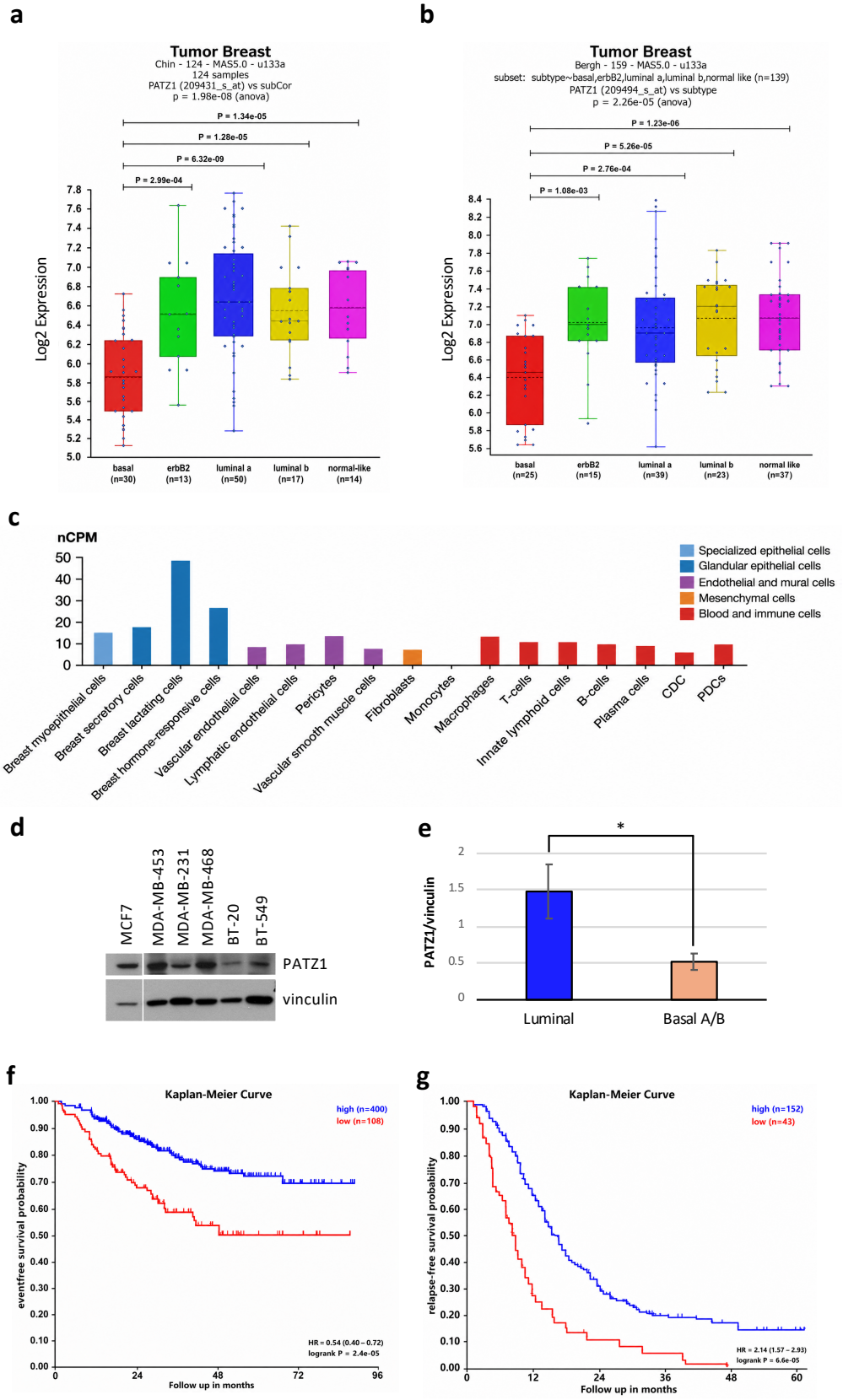
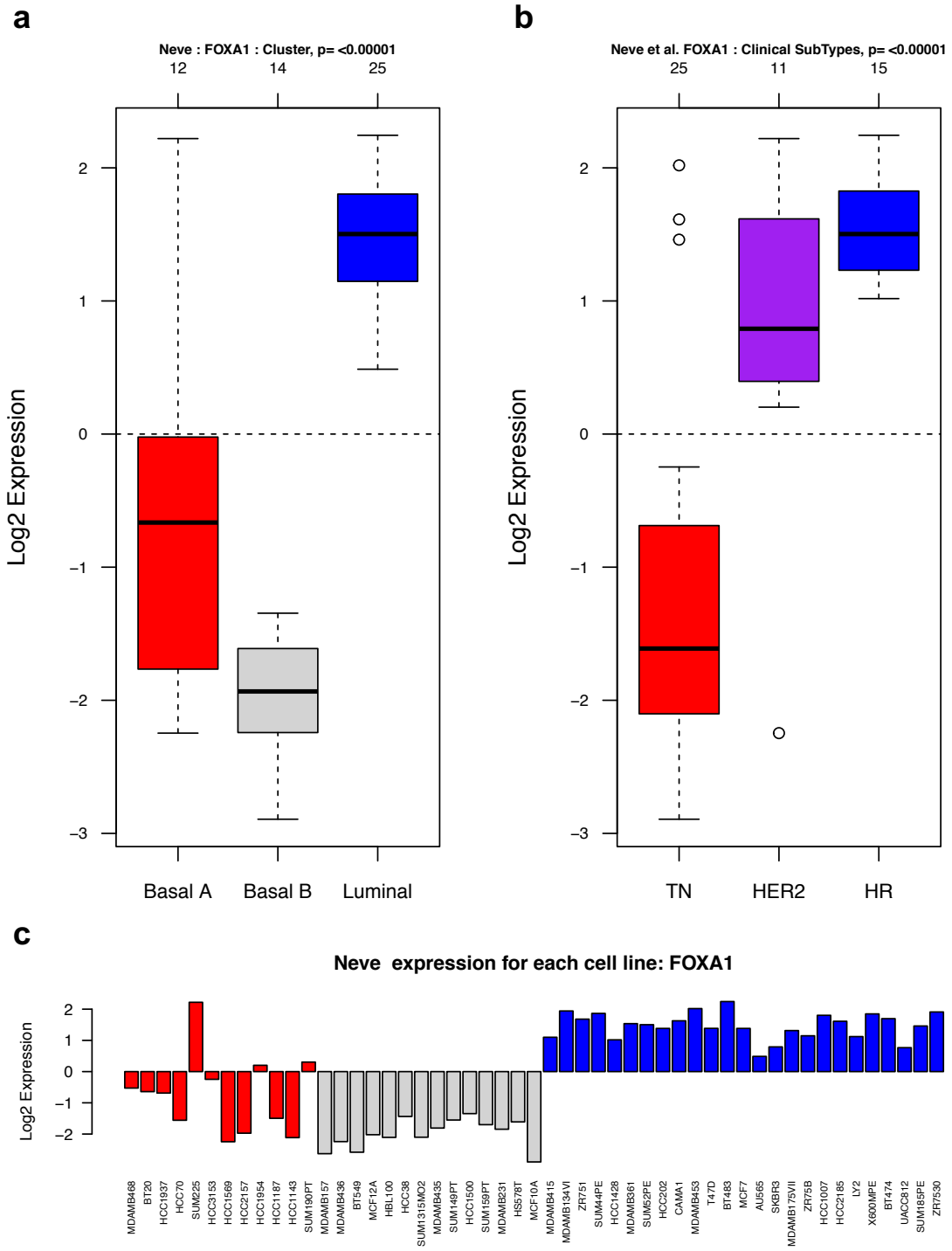
PATZ1 Restrains Basal-like Breast Cancer Aggressiveness while Preserving FOXA1-Driven Luminal Identity

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Supp. Fig.1 Additional evidence supporting the association of PATZ1 expression with luminal breast cancer identity and favorable clinical outcome. Analyses in panels **a**, **b**, **f** and **g** were performed using the R2: Genomics Analysis and Visualization Platform. **(a, b)** PATZ1 mRNA expression across breast cancer molecular subtypes in two independent breast cancer datasets (GSE60031, **a**; GSE1456, **b**), showing higher PATZ1 expression in luminal than in basal tumors. **(c)** Single-cell RNA-sequencing analysis of PATZ1 expression across cell populations of normal human breast tissue using the Human Protein Atlas. Expression levels are reported as normalized counts per million (nCPM). The highest PATZ1 expression was observed in breast lactating and hormone-responsive cells (approximately 48 and 27 nCPM, respectively), followed by breast secretory and myoepithelial cells. Cell populations are color-coded according to the Human Protein Atlas cell-type classification. **(d)** Representative Western blot analysis of PATZ1 protein expression in luminal (MCF7 and MDA-MB-453) and basal-like (MDA-MB-231, MDA-MB-468, BT-20 and BT-549) breast cancer cell lines. Vinculin was used as a loading control. **(e)** Densitometric quantification of PATZ1 protein levels normalized to vinculin, showing higher PATZ1 expression in luminal than basal-like breast cancer cell lines. Data are presented as mean ± SEM. **(f, g)** Kaplan–Meier analysis of event-free survival (EFS) in the GSE25066 cohort (**f**) and relapse-free survival (RFS) in the GSE29271 cohort (**g**), showing improved outcome in patients with high *PATZ1* expression.



Supp. Fig.2. FOXA1 expression is enriched in luminal breast cancer cell lines. Gene expression analyses were performed using the GOBO breast cancer gene expression platform.
(a) *FOXA1* mRNA expression according to the molecular classification of the Neve breast cancer cell line panel (Basal A, Basal B and Luminal), showing significantly higher *FOXA1* expression in luminal cell lines. **(b)** *FOXA1* mRNA expression according to the clinical subtype classification of the Neve breast cancer cell line panel (triple-negative, HER2-positive and hormone receptor-positive), showing preferential *FOXA1* expression in hormone receptor-positive cell lines. **(c)** *FOXA1* mRNA expression across individual breast cancer cell lines in the Neve dataset.